

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

- (i) APPLICANT: Ryazanov, Alexey G.
Hait, William N.
Pavur, Karen S.

10

- (ii) TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
AND METHODS OF USE THEREFOR

- (iii) NUMBER OF SEQUENCES: 25

15

- (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: David A. Jackson, Esq.
(B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

20

- (v) COMPUTER READABLE FORM:

25

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30

- (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

35

- (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742

(C) REFERENCE/DOCKET NUMBER: 601-1-078

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-487-5800

5

(B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2178 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCAGACG AAGACCTCAT CTTCCGCCTG GAAGGTGTTG ATGGCGGCCA GTCCCCCCGA 60

GCTGGCCATG ATGGTGATTC TGATGGGGAC AGCGACGATG AGGAAGGTTA CTTTCATCTGC 120

30

CCCATCACGG ATGACCCAAG CTCGAACCAG AATGTCAATT CCAAGGTAA TAAGTACTAC 180

AGCAACCTAA CAAAAAGTGA GCGGTATAGC TCCAGCGGGT CCCC GGCAA CTCCTTCCAC 240

35 TTCAAGGAAG CCTGGAAGCA CGCAATCCAG AAGGCCAAGC ACATGCCCCG CCCCTGGGCT 300

GAGTTCCACC TGGAAGATAT TGCCACCGAA CGTGCTACTC GACACAGGTA CAACGCCGTC 360

	ACCGGGGAAT GGCTGGATGA TGAAGTTCTG ATCAAGATGG CATCTCAGCC CTTCGGCCGA	420
	GGAGCAATGA GGGAGTGCTT CCGGACGAAG AAGCTCTCCA ACTTCTTGCA TGCCCAGCAG	480
5	TGGAAGGGCG CCTCCAATA CGTGGCGAAG CGCTACATCG AGCCCGTAGA CCGGGATGTG	540
	TACTTTGAGG ACGTGCGTCT ACAGATGGAG GCCAAGCTCT GGGGGGAGGA GTATAATCGG	600
	CACAAGCCCC CCAAGCAGGT GGACATCATG CAGATGTGCA TCATCGAGCT GAAGGACAGA	660
10	CCGGGCAAGC CCCTCTTCCA CCTGGAGCAC TACATCGAGG GCAAGTACAT CAAGTACAAC	720
	TCCAACCTCTG GCTTTGTCCG TGATGACAAC ATCCGACTGA CGCCGCAGGC CTTCAGCCAC	780
15	TTCACTTTTG AGCGTTCCGG CCATCAGCTG ATAGTGGTGG ACATCCAGGG AGTTGGGGAT	840
	CTCTACACTG ACCCACAGAT CCACACGGAG ACGGGCACTG ACTTTGGAGA CGGCAACCTA	900
	GGTGTCCGCG GGATGGCGCT CTTCTTCTAC TCTCATGCCT GCAACCGGAT TTGCGAGAGC	960
20	ATGGGCGCTTG CTCCCTTTGA CCTCTCGCCC CGGGAGAGGG ATGCAGTGAA TCAGAACACC	1020
	AAGCTGCTGC AATCAGCCAA GACCATCTTG AGAGGAACAG AGGAAAAATG TGGGAGCCCC	1080
25	CGAGTAAGGA CCCTCTCTGG GAGCCGGCCA CCCCTGCTCC GTCCCCTTTC AGAGAACTCT	1140
	GGAGACGAGA ACATGAGCGA CGTGACCTTC GACTCTCTCC CTTCTTCCCC ATCTTCGGCC	1200
	ACACCACACA GCCAGAAGCT AGACCACCTC CATTGGCCAG TGTTCACTGA CCTCGATAAC	1260
30	ATGGCATCCA GAGACCATGA TCATCTAGAC AACCACCGGG AGTCTGAGAA TAGTGGGGAC	1320
	AGCGGATACC CCAGTGAGAA GCGGGGTGAG CTGGATGACC CTGAGCCCCG AGAACATGGC	1380
35	CACTCATACA GTAATCGGAA GTACGAGTCT GACGAAGACA GCCTGGGCAG CTCTGGACGG	1440
	GTATGTGTAG AGAAGTGGA TCTCCTCAAC TCCTCCCGCC TCCACCTGCC GAGGGCTTCG	1500

GCCGTGGCCC TGGAAGTGCA AAGGCTTAAT GCTCTGGACC TCGAAAAGAA AATCGGGAAG 1560
 TCCATTTTGG GGAAGGTCCA TCTGGCCATG GTGCGCTACC ACGAGGGTGG GCGCTTCTGC 1620
 5 GAGAAGGGCG AGGAGTGGGA CCAGGAGTCG GCTGTCTTCC ACCTGGAGCA CGCAGCCAAC 1680
 CTGGGCGAGC TGGAGGCCAT CGTGGGCCTG GGACTCATGT ACTCGCAGTT GCCTCATCAC 1740
 ATCCTAGCCG ATGTCTCTCT GAAGGAGACA GAAGAGAACA AAACCAAAGG ATTTGATTAC 1800
 10 TTACTAAAGG CCGCTGAAGC TGGCGACAGG CAGTCCATGA TCCTAGTGGC GCGAGCTTTT 1860
 GACTCTGGCC AGAACCTCAG CCCGGACAGG TGCCAAGACT GGCTAGAGGC CCTGCACTGG 1920
 15 TACAACACTG CCCTGGAGAT GACGGACTGT GATGAGGGCG GTGAGTACGA CGGAATGCAG 1980
 GACGAGCCCC GGTACATGAT GCTGGCCAGG GAGGCAGAGA TGCTGTTTAC AGGAGGCTAC 2040
 GGGCTGGAGA AGGACCCGCA GAGATCAGGG GACTTGTATA CCCAGGCAGC AGAGGCAGCG 2100
 20 ATGGAAGCCA TGAAGGGCCG ACTGGCCAAC CAGTACTACC AAAAGGCTGA AGAGGCCTGG 2160
 GCCCAGATGG AGGAATAA 2178

25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 725 amino acids
 (B) TYPE: amino acid
 30 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Asp Glu Asp Leu Ile Phe Arg Leu Glu Gly Val Asp Gly Gly
 1 5 10 15

Gln Ser Pro Arg Ala Gly His Asp Gly Asp Ser Asp Gly Asp Ser Asp
 20 25 30

Asp Glu Glu Gly Tyr Phe Ile Cys Pro Ile Thr Asp Asp Pro Ser Ser
 35 40 45

Asn Gln Asn Val Asn Ser Lys Val Asn Lys Tyr Tyr Ser Asn Leu Thr
 50 55 60

Lys Ser Glu Arg Tyr Ser Ser Ser Gly Ser Pro Ala Asn Ser Phe His
 20 65 70 75 80

Phe Lys Glu Ala Trp Lys His Ala Ile Gln Lys Ala Lys His Met Pro
 85 90 95

Asp Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala Thr Glu Arg Ala
 100 105 110

Thr Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp Leu Asp Asp Glu
 115 120 125

Val Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg Gly Ala Met Arg
 30 130 135 140

Glu Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu His Ala Gln Gln
 35 145 150 155 160

Trp Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr Ile Glu Pro Val

	165	170	175
	Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln Met Glu Ala Lys		
	180	185	190
5	Leu Trp Gly Glu Glu Tyr Asn Arg His Lys Pro Pro Lys Gln Val Asp		
	195	200	205
	Ile Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg Pro Gly Lys Pro		
10	210	215	220
	Leu Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr Ile Lys Tyr Asn		
	225	230	235 240
15	Ser Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg Leu Thr Pro Gln		
	245	250	255
	Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His Gln Leu Ile Val		
	260	265	270
20	Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp Pro Gln Ile His		
	275	280	285
	Thr Glu Thr Gly Thr Asp Phe Gly Asp Gly Asn Leu Gly Val Arg Gly		
25	290	295	300
	Met Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg Ile Cys Glu Ser		
	305	310	315 320
30	Met Gly Leu Ala Pro Phe Asp Leu Ser Pro Arg Glu Arg Asp Ala Val		
	325	330	335
	Asn Gln Asn Thr Lys Leu Leu Gln Ser Ala Lys Thr Ile Leu Arg Gly		
	340	345	350
35	Thr Glu Glu Lys Cys Gly Ser Pro Arg Val Arg Thr Leu Ser Gly Ser		
	355	360	365

	Arg	Pro	Pro	Leu	Leu	Arg	Pro	Leu	Ser	Glu	Asn	Ser	Gly	Asp	Glu	Asn	
	370						375						380				
5	Met	Ser	Asp	Val	Thr	Phe	Asp	Ser	Leu	Pro	Ser	Ser	Pro	Ser	Ser	Ala	
	385						390				395					400	
	Thr	Pro	His	Ser	Gln	Lys	Leu	Asp	His	Leu	His	Trp	Pro	Val	Phe	Ser	
					405					410					415		
10	Asp	Leu	Asp	Asn	Met	Ala	Ser	Arg	Asp	His	Asp	His	Leu	Asp	Asn	His	
				420					425					430			
	Arg	Glu	Ser	Glu	Asn	Ser	Gly	Asp	Ser	Gly	Tyr	Pro	Ser	Glu	Lys	Arg	
15				435				440					445				
	Gly	Glu	Leu	Asp	Asp	Pro	Glu	Pro	Arg	Glu	His	Gly	His	Ser	Tyr	Ser	
	450						455					460					
	Asn	Arg	Lys	Tyr	Glu	Ser	Asp	Glu	Asp	Ser	Leu	Gly	Ser	Ser	Gly	Arg	
20	465					470					475					480	
	Val	Cys	Val	Glu	Lys	Trp	Asn	Leu	Leu	Asn	Ser	Ser	Arg	Leu	His	Leu	
					485					490					495		
25	Pro	Arg	Ala	Ser	Ala	Val	Ala	Leu	Glu	Val	Gln	Arg	Leu	Asn	Ala	Leu	
					500					505					510		
	Asp	Leu	Glu	Lys	Lys	Ile	Gly	Lys	Ser	Ile	Leu	Gly	Lys	Val	His	Leu	
			515					520					525				
30	Ala	Met	Val	Arg	Tyr	His	Glu	Gly	Gly	Arg	Phe	Cys	Glu	Lys	Gly	Glu	
		530						535				540					
	Glu	Trp	Asp	Gln	Glu	Ser	Ala	Val	Phe	His	Leu	Glu	His	Ala	Ala	Asn	
35	545					550					555					560	
	Leu	Gly	Glu	Leu	Glu	Ala	Ile	Val	Gly	Leu	Gly	Leu	Met	Tyr	Ser	Gln	

565

570

575

Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys Glu Thr Glu Glu
580 585 590

5

Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala Ala Glu Ala Gly
595 600 605

10

Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe Asp Ser Gly Gln
610 615 620

Asn Leu Ser Pro Asp Arg Cys Gln Asp Trp Leu Glu Ala Leu His Trp
625 630 635 640

15

Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu Gly Gly Glu Tyr
645 650 655

Asp Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu Ala Arg Glu Ala
660 665 670

20

Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys Asp Pro Gln Arg
675 680 685

Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala Met Glu Ala Met
690 695 700

25

Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys Ala Glu Glu Ala Trp
705 710 715 720

30

Ala Gln Met Glu Glu
725

(2) INFORMATION FOR SEQ ID NO:3:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2175 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15 ATGGCAGACG AAGACCTCAT CTTCTGCCTG GAAGGTGTTG ACGGTGGCAG GTGCTCCCGA 60
GCTGGCCACA ATGCGGACTC TGACACAGAC AGTGACGATG ATGAGGGCTA TTTCATCTGC 120
CCCATCACTG ATGACCACAT GTCCAATCAG AATGTCAGCT CCAAAGTCCA GAGCTACTAT 180
20 AGCAACCTAA CAAAAACAGA GTGCGGCTCC ACAGGGTCAC CAGCCAGCTC CTTCCACTTC 240
AAGGAAGCCT GGAAGCATGC GATCGAGAAA GCCAAGCACA TGCCTGACCC CTGGGCTGAA 300
25 TTCCATCTCG AGGACATCGC CACAGAAAT GCTACTCGGC ACAGGTACAA CGCTGTCACC 360
GGGGAATGGC TGAAAGACGA GGTTCCTGATC AAGATGGCGT CTCAGCCCTT CGGCCGTGGA 420
GCAATGAGGG AGTGCTTCAG GACGAAGAAA CTCTCCAAC TCTTGACGC CCAGCAATGG 480
30 AAGGGGGCCT CCAACTACGT GGCCAAGCGC TACATCGAGC CGGTGGACAG GAGCGTGTAC 540
TTTGAGGATG TGCAGCTCCA GATGGAGGCG AAGCTCTGGG GGGAGGATTA CAATCGGCAC 600
35 AAGCCCCCCA AGCAGGTGGA TATCATGCAG ATGTGCATCA TTGAGCTAAA GGACAGACCA 660
GGCCAGCCCC TCTTCCACTT GGAGCACTAC ATTGAGGGCA AGTACATCAA GTACAATTCC 720

	AACTCAGGCT TTGTCCGTGA TGACAACATC CGACTAACCC CACAGGCCTT CAGCCATTTC	780
	ACATTTGAGC GTTCTGGTCA TCAGCTGATT GTAGTGGACA TCCAGGGTGT GGGTGACCTT	840
5	TATACCGACC CACAGATCCA CACTGAGAAA GGCCTGACT TTGGAGATGG TAACCTTGGT	900
	GTCCGGGGAA TGGCTCTCTT CTTCTACTCT CATGCCTGCA ACCGGATTG TCAGAGCATG	960
	GGCCTTACGC CCTTTGACCT CTCCCCACGG GAACAGGATG CGGTGAATCA GAGCACCAGG	1020
10	CTATTGCAAT CAGCCAAGAC CATCTTGAGG GGGACAGAGG AGAAGTGTGG GAGTCCCCGC	1080
	ATAAGGACAC TCTCTAGCAG CCGGCCCCCT TTGCTCCTT GCCTGTCAGA GAACTCCGGG	1140
15	GATGAGAACA TGAGTGACGT GACCTTTGAC TCTCTGCCTT CCTCCCCGTC TTCAGCTACA	1200
	CCACACAGCC AGAAACTGGA CCACCTCCAT TGGCCAGTGT TTGGTGACCT CGATAACATG	1260
	GGCCCTAGAG ACCATGACCG TATGGACAAT CACCGGGACT CTGAGAATAG TGGGGACAGT	1320
20	GGGTATCCAA GCGAGAAGCG AAGTGACCTG GATGATCCTG AGCCCCGAGA ACACGGCCAC	1380
	TCCAACGGCA ACCGAAGGCA TGAATCTGAC GAGGATAGCC TGGGCAGCTC TGGACGGGTC	1440
25	TGTGTGGAGA CGTGGAACCT GCTCAATCCC TCCCGCCTGC ACCTGCCGAG GCCCTCGGCC	1500
	GTGGCCCTAG AAGTGCAGAG GCTAAATGCC CTGGACCTTG GAAGGAAAAT CGGGAAGTCT	1560
	GTTTTGGGGA AAGTCCATTT GGCCATGGTG CGATACCACG AGGGCGGGCG CTTCTGCGAG	1620
30	AAGGATGAGG AGTGGGATCG AGAGTCAGCC ATCTTCCATC TGGAGCATGC AGCTGACCTG	1680
	GGAGAACTGG AGGCCATCGT GGGCCTAGGC CTCATGTACT CTCAGCTGCC CCACCACATC	1740
35	CTGGCTGATG TCTCTCTGAA GGAGACAGAG GAGAACAAGA CAAAAGGCTT TGATTACTTA	1800
	CTGAAGGCGG CAGAAGCTGG TGACAGGCAT TCCATGATTT TAGTGGCCCG AGCTTTTGAC	1860

ACTGGCCTGA ACCTCAGCCC AGACAGGTGT CAAGACTGGT CGGAAGCCTT GCACTGGTAC 1920
 AACACAGCCC TGGAGACAAC AGACTGCGAT GAAGGCGGGG AGTACGATGG GATACAGGAC 1980
 5 GAGCCCCAGT ACGCACTGCT GGCCAGGGAG GCGGAGATGC TGCTCACCGG GGGATTGGA 2040
 CTGGACAAGA ACCCCCCAAG ATCAGGAGAT TTGTACACCC AGGCAGCTGA GGCAGCAATG 2100
 GAAGCCATGA AGGGCCGGCT AGCCAACCAG TACTACGAGA AGGCGGAAGA GGCCTGGGCC 2160
 10 CAGATGGAGG AATAA 2175

(2) INFORMATION FOR SEQ ID NO:4:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 724 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

25 (vi) ORIGINAL SOURCE: ..
 (A) ORGANISM: Mus musculus

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Asp Glu Asp Leu Ile Phe Cys Leu Glu Gly Val Asp Gly Gly
 1 5 10 15

35 Arg Cys Ser Arg Ala Gly His Asn Ala Asp Ser Asp Thr Asp Ser Asp
 20 25 30

	Asp Asp Glu Gly Tyr Phe Ile Cys Pro Ile Thr Asp Asp His Met Ser
	35 40 45
5	Asn Gln Asn Val Ser Ser Lys Val Gln Ser Tyr Tyr Ser Asn Leu Thr
	50 55 60
	Lys Thr Glu Cys Gly Ser Thr Gly Ser Pro Ala Ser Ser Phe His Phe
	65 70 75 80
10	Lys Glu Ala Trp Lys His Ala Ile Glu Lys Ala Lys His Met Pro Asp
	85 90 95
	Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala Thr Glu His Ala Thr
	100 105 110
15	Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp Leu Lys Asp Glu Val
	115 120 125
	Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg Gly Ala Met Arg Glu
20	130 135 140
	Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu His Ala Gln Gln Trp
	145 150 155 160
25	Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr Ile Glu Pro Val Asp
	165 170 175
	Arg Ser Val Tyr Phe Glu Asp Val Gln Leu Gln Met Glu Ala Lys Leu
	180 185 190
30	Trp Gly Glu Asp Tyr Asn Arg His Lys Pro Pro Lys Gln Val Asp Ile
	195 200 205
	Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg Pro Gly Gln Pro Leu
35	210 215 220
	Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr Ile Lys Tyr Asn Ser

	225		230		235		240
	Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg Leu Thr Pro Gln Ala						
		245		250		255	
5	Phe Ser His Phe Thr Phe Glu Arg Ser Gly His Gln Leu Ile Val Val						
		260		265		270	
	Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp Pro Gln Ile His Thr						
10		275		280		285	
	Glu Lys Gly Thr Asp Phe Gly Asp Gly Asn Leu Gly Val Arg Gly Met						
		290		295		300	
15	Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg Ile Cys Gln Ser Met						
		305		310		315	320
	Gly Leu Thr Pro Phe Asp Leu Ser Pro Arg Glu Gln Asp Ala Val Asn						
		325		330		335	
20	Gln Ser Thr Arg Leu Leu Gln Ser Ala Lys Thr Ile Leu Arg Gly Thr						
		340		345		350	
	Glu Glu Lys Cys Gly Ser Pro Arg Ile Arg Thr Leu Ser Ser Ser Arg						
25		355		360		365	
	Pro Pro Leu Leu Leu Arg Leu Ser Glu Asn Ser Gly Asp Glu Asn Met						
		370		375		380	
30	Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser Pro Ser Ser Ala Thr						
		385		390		395	400
	Pro His Ser Gln Lys Leu Asp His Leu His Trp Pro Val Phe Gly Asp						
		405		410		415	
35	Leu Asp Asn Met Gly Pro Arg Asp His Asp Arg Met Asp Asn His Arg						
		420		425		430	

	Asp Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro Ser Glu Lys Arg Ser
	435 440 445
5	Asp Leu Asp Asp Pro Glu Pro Arg Glu His Gly His Ser Asn Gly Asn
	450 455 460
	Arg Arg His Glu Ser Asp Glu Asp Ser Leu Gly Ser Ser Gly Arg Val
	465 470 475 480
10	Cys Val Glu Thr Trp Asn Leu Leu Asn Pro Ser Arg Leu His Leu Pro
	485 490 495
	Arg Pro Ser Ala Val Ala Leu Glu Val Gln Arg Leu Asn Ala Leu Asp
	500 505 510
15	Leu Gly Arg Lys Ile Gly Lys Ser Val Leu Gly Lys Val His Leu Ala
	515 520 525
	Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys Glu Lys Asp Glu Glu
20	530 535 540
	Trp Asp Arg Glu Ser Ala Ile Phe His Leu Glu His Ala Ala Asp Leu
	545 550 555 560
25	Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu Met Tyr Ser Gln Leu
	565 570 575
	Pro His His Ile Leu Ala Asp Val Ser Leu Lys Glu Thr Glu Glu Asn
	580 585 590
30	Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala Ala Glu Ala Gly Asp
	595 600 605
	Arg His Ser Met Ile Leu Val Ala Arg Ala Phe Asp Thr Gly Leu Asn
35	610 615 620
	Leu Ser Pro Asp Arg Cys Gln Asp Trp Ser Glu Ala Leu His Trp Tyr

625 630 635 640

Asn Thr Ala Leu Glu Thr Thr Asp Cys Asp Glu Gly Gly Glu Tyr Asp
645 650 655

5

Gly Ile Gln Asp Glu Pro Gln Tyr Ala Leu Leu Ala Arg Glu Ala Glu
660 665 670

10

Met Leu Leu Thr Gly Gly Phe Gly Leu Asp Lys Asn Pro Gln Arg Ser
675 680 685

Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala Met Glu Ala Met Lys
690 695 700

15

Gly Arg Leu Ala Asn Gln Tyr Tyr Glu Lys Ala Glu Glu Ala Trp Ala
705 710 715 720

Gln Met Glu Glu

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 3465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Dictyostelium discoideum

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	ATGTTTAATA TAAAAAGAG AAAAGAGAGT ATAACAGGTA TACCACCAAT AAATGTTAAT	60
5	AGTCCACAAT CAGTTCCATT GAGTGAACA TTGCAATCAC CATTGATTAC ACCAAATTCA	120
	CCAAATTTTG TTTCACGTCA ATGTCCATTG AAAAAGTTTG GATGTAGTAG TTTTGTAGTT	180
	TCAAAGGCAG AGTTTGATAA TCACTTAAAG GATGACGCAC AATTCATTT ACAATTGGCA	240
10	GTGGAGAAAT TTGATCATCA ATTTGATTTA CACACACAAT TGATGGCACA TTTTACTGAG	300
	CAAATGGAGG ATCAATTAGA GAAAACAATG AAGGTCGTAC GTAATCATAC AGATAGTTTA	360
15	GGCGGTAATG TTCAAACCAA ATTGGATGAA GGCATTGAAA AATGTATGGC TTTTGCTAAA	420
	AAGGTTGAAC AACAACAACA ACAATTGGCC AAAAGATTAA TCACTCAACA AATTCAAGAG	480
	AAGAAATCAA CCTCTTCACC TTTAGTTAAA GGTGGTATTA GTGGTGGTGG TGGTAGTGGT	540
20	GGCGATGATT CTTTGTATGG CGCAAATATA TCATCAATGT CAACTAGTAA ACAAGAATTA	600
	CAACAAGAAT TACAATCATT ATCAATTAAA ATGAAAAAAG AATTGACAGA ATTATCCGAT	660
25	GAAGGTGAAG TTAATGAAAA GATTGATAAA CGTCAATTGG TCTCTACGAT CGATGATTCA	720
	ATTGGAAAGA AACAGATTG CATCGGTTAT ACATTGGAGA GTTCAATCAT TAAAAAGGTT	780
30	GAAGAGAAAG AGAAAAAGAA ATCCGAACAA AATCAACTTC TCTTTGATTC AAAGATTGAA	840
	TCCTTAAAAG ATAAGATTAA AATCATTGAA ACTCAACAAT TGGATACTTC ATCAGAGGTT	900
	AGAAAATTGA AATTAGAAAG TACAAGTAGT GGAAATTTAA TGGCAGGTCT TAATGGTACC	960
35	TCTGGTAGAC CTTTCATCATC TTCTCACTTT ATTCCATCCT CTGTTTCTGC CGCTGCTAAC	1020
		1080

	AATATCAACA AGAATGAAAT CATGGAAGAG GTTAAAAAGG TAGAAGAGAA ACTTCAAAAG	1140
	AAAATTCGTG AAGAGATTGA TAATACAAAA GCTGAACTCT CAAAGGTTGA ACGTTCCGTT	1200
5	AAAGATAATC GTAGTGAAAT TGAAGGTTTG GAAAAAGATT GTAAGAATCA ATTCGATAAA	1260
	CAAGACAATA AGATCAAACA AGTTGAGGAT GATTTGAAAA AGAGTGATTC ATTACTTTTG	1320
	TTAATGCAAA ATAACCTCAA GAAATATAAT GAATTTGTTG ATAGAGAACG TGATCGTGAA	1380
10	AGTGAACGTT TGAAACTTCA AGATTCTATC AAACGTTTAG AACAAAATCA AAAGAAAATC	1440
	GAAGCTGAAA TTCAAGAAGG TAATGAACAA GTTGAACGTG TTTTACGTGA GGAAGCTTCA	1500
15	ATCTCACCAA TTAGTTCAGT TCCAAAATCA CCAATCACAA CCAAACGTC ATCGATTATT	1560
	TTAAATTCAC CACCAATGAC TTCACAACAA TCATCACCAA AGATTCAAGA TCTTCTCTCA	1620
	AGTAGTGGTA GTAGTAGTGT TAGTGGTATA AATATTTCTT CTGAAACCGG TGAAATGGGT	1680
20	ATTCTTTGGG AATTTGATCC AATCATTAAC AAATGGATTA GATTATCAAT GAAGCTAAAG	1740
	GTAGAAAGAA AACCATTTGC AGAGGGTGCT CTTAGAGAGG CTTATCATAC CGTTTCATTG	1800
25	GGTGTGGAA CCGATGAAAA TTATCCATTA GGTACAACCA CCAATTATT CCCACCAATT	1860
	GAAATGATTT CACCAATTTT AAAGAATAAT GAGGCAATGA CTCAATTGAA GAATGGTACA	1920
	AAATTTGTTT TGAAACTCTA CAAAAAGGAA GCTGAACAAC AAGCTAGCAG AGAATTATAC	1980
30	TTTGAAGATG TTAAAATGCA AATGGTCTGT AGAGATTGGG GTAATAAATT CAATCAAAAAG	2040
	AAACCACCAA AGAAAATTGA ATTCCTTATG TCTTGGGTTG TAGAGTTAAT CGATAGATCT	2100
35	CCTTCTTCCA ATGGTCAACC AATACTTTGT TCCATTGAAC CATTATTGGT TGGTGAATTC	2160
	AAAAAGAATA ATTCAAATTA TGGTGCAGTT TTAACCAATC GTTCAACTCC ACAAGCATTCT	2220

	TCTCATTTCA CCTATGAACT CTCAAATAAA CAAATGATCG TTGTCGATAT TCAAGGTGTT	2280
	GATGATCTTT ACACTGATCC TCAAATTCAT ACACCCGATG GTAAAGGATT TGGTCTTGGT	2340
5	AATCTTGGTA AAGCAGGTAT CAATAAATTC ATCACCACCTC ACAAATGTAA TGCTGTTTGT	2400
	GCTCTTTTAG ATTTAGATGT TAAATTGGGT GGTGTACTAT CTGGAAATAA TAAGAAACAA	2460
	CTTCAACAAG GTACTATGGT TATGCCAGAT ATTCTCCCAG AACTTATGCC ATCTGATAAC	2520
10	ACCATTAAAG TGGGTGCAAA ACAACTTCCA AAAGCTGAAT TCTCAAAGAA AGATCTCAAA	2580
	TGTGTTAGCA CCATTCAAAG TTTCCGTGAA CGTGTTAACT CGATCGCATT CTTTGATAAT	2640
15	CAAAAGTTAT TATGCGCTGG TTATGGTGAT GGTACCTATA GAGTTTTCGA TGTCAATGAC	2700
	AATTGGAAAT GTTTATACAC TGTCAATGGT CATAGAAAAT CAATTGAAAG TATCGCTTGT	2760
	AATAGTAATT ACATTTTCAC TTCATCACCT GATAACACCA TCAAAGTTCA TATCATTCGT	2820
20	AGTGGTAACA CCAAATGTAT AGAGACATTG GTTGGTCACA CTGGTGAAGT TAATTGTGTC	2880
	GTGGCCAATG AAAAATATCT TTTCAGTTGT AGTTATGATA AAACATATCA GGTGTTGGGAT	2940
25	TTGTCAACCT TTAAAGAAAT TAAATCATT T GAGGGTGTTT ATACAAAGTA CATTAAACA	3000
	TTGGCTTTGA GTGGACGTTA TCTTTTTAGT GGTGGTAACG ATCAAATCAT TTACGTTTGG	3060
	GATACTGAAA CACTTAGTAT GCTTTTCAAT ATGCAAGGTC ATGAAGATTG GGTACTCTCT	3120
30	CTTCATTGTA CCGCTAGTTA TCTTTTCTCA ACCTCAAAG ATAATGTCAT CAAGATTG	3180
	GATCTCTCAA ATTTAGTTG TATCGATACT CTAAAAGGTC ATTGGAATTC TGTCTCAAGT	3240
35	TGTGTCGTAA AAGATCGTTA TCTATACAGT GGTCTGAAG ATAATTCAAT CAAAGTTTGG	3300
	GATCTCGATA CACTTGAATG TGTTTACACC ATTCCAAAAT CTCATTCTTT GGGTGTAATA	3360

TGTTTAATGG TTTTCAATAA TCAAATCATT TCTGCTGCTT TCGATGGTTC AATTAAAGTT 3420

TGGGAATGGC AATCGAAATA ATCTTTGTAA ATTTTGTGTA AAAAA 3465

5 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: Dictyostelium discoideum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

25 Met Phe Asn Ile Lys Lys Arg Lys Glu Ser Ile Thr Gly Ile Pro Pro
1 5 .. 10 15

Ile Asn Val Asn Ser Pro Gln Ser Val Pro Leu Ser Gly Thr Leu Gln
20 25 30

30 Ser Pro Leu Ile Thr Pro Asn Ser Pro Asn Phe Val Ser Arg Gln Cys
35 40 45

Pro Phe Lys Lys Phe Gly Cys Ser Ser Phe Leu Val Ser Lys Ala Glu
50 55 60

35 Phe Asp Asn His Leu Lys Asp Asp Ala Gln Phe His Leu Gln Leu Ala
65 70 75 80

	Val Glu Lys Phe Asp His Gln Phe Asp Leu His Thr Gln Leu Met Ala	
	85	90 95
5	His Phe Thr Glu Gln Met Glu Asp Gln Leu Glu Lys Thr Met Lys Val	
	100	105 110
	Val Arg Asn His Thr Asp Ser Leu Gly Gly Asn Val Gln Thr Lys Leu	
	115	120 125
10	Asp Glu Gly Ile Glu Lys Cys Met Ala Phe Ala Lys Lys Val Glu Gln	
	130	135 140
	Gln Gln Gln Gln Leu Ala Lys Arg Leu Ile Thr Gln Gln Ile Gln Glu	
	145	150 155 160
15	Lys Lys Ser Thr Ser Ser Pro Leu Val Lys Gly Gly Ile Ser Gly Gly	
	165	170 175
	Gly Gly Ser Gly Gly Asp Asp Ser Phe Asp Gly Ala Asn Ile Ser Ser	
20	180	185 190
	Met Ser Thr Ser Lys Gln Glu Leu Gln Gln Glu Leu Gln Ser Leu Ser	
	195	200 205
25	Ile Lys Met Lys Lys Glu Leu Thr Glu Leu Ser Asp Glu Leu Ser Gln	
	210	215 220
	Lys Leu Glu Arg Ser Thr Gly Asn Ile Asp Ile Lys Ile Lys Arg Ile	
	225	230 235 240
30	Glu Gly Glu Val Asn Glu Lys Ile Asp Lys Arg Gln Leu Val Ser Thr	
	245	250 255
	Ile Asp Asp Ser Ile Gly Lys Lys Thr Asp Ser Ile Gly Tyr Thr Leu	
35	260	265 270
	Glu Ser Ser Ile Ile Lys Lys Val Glu Glu Lys Glu Lys Lys Lys Ser	

[illegible]

	Glu Ala Glu Ile Gln Glu Gly Asn Glu Gln Val Glu Arg Val Leu Arg	
	485	490 495
5	Glu Glu Ala Ser Ile Ser Pro Ile Ser Ser Val Pro Lys Ser Pro Ile	
	500	505 510
	Thr Thr Lys Arg Ser Ser Ile Ile Leu Asn Ser Pro Pro Met Thr Ser	
	515	520 525
10	Gln Gln Ser Ser Pro Lys Ile Gln Asp Leu Leu Ser Ser Ser Gly Ser	
	530	535 540
	Ser Ser Val Ser Gly Ile Asn Ile Ser Ser Glu Thr Gly Glu Met Gly	
	545	550 555 560
15	Ile Leu Trp Glu Phe Asp Pro Ile Ile Asn Lys Trp Ile Arg Leu Ser	
	565	570 575
	Met Lys Leu Lys Val Glu Arg Lys Pro Phe Ala Glu Gly Ala Leu Arg	
20	580	585 590
	Glu Ala Tyr His Thr Val Ser Leu Gly Val Gly Thr Asp Glu Asn Tyr	
	595	600 605
25	Pro Leu Gly Thr Thr Thr-Lys Leu Phe Pro Pro Ile Glu Met Ile Ser	
	610	615 620
	Pro Ile Ser Lys Asn Asn Glu Ala Met Thr Gln Leu Lys Asn Gly Thr	
	625	630 635 640
30	Lys Phe Val Leu Lys Leu Tyr Lys Lys Glu Ala Glu Gln Gln Ala Ser	
	645	650 655
	Arg Glu Leu Tyr Phe Glu Asp Val Lys Met Gln Met Val Cys Arg Asp	
35	660	665 670
	Trp Gly Asn Lys Phe Asn Gln Lys Lys Pro Pro Lys Lys Ile Glu Phe	

675

680

685

5 Leu Met Ser Trp Val Val Glu Leu Ile Asp Arg Ser Pro Ser Ser Asn
 690 695 700

Gly Gln Pro Ile Leu Cys Ser Ile Glu Pro Leu Leu Val Gly Glu Phe
 705 710 715 720

10 Lys Lys Asn Asn Ser Asn Tyr Gly Ala Val Leu Thr Asn Arg Ser Thr
 725 730 735

Pro Gln Ala Phe Ser His Phe Thr Tyr Glu Leu Ser Asn Lys Gln Met
 740 745 750

15 Ile Val Val Asp Ile Gln Gly Val Asp Asp Leu Tyr Thr Asp Pro Gln
 755 760 765

20 Ile His Thr Pro Asp Gly Lys Gly Phe Gly Leu Gly Asn Leu Gly Lys
 770 775 780

Ala Gly Ile Asn Lys Phe Ile Thr Thr His Lys Cys Asn Ala Val Cys
 785 790 795 800

25 Ala Leu Leu Asp Leu Asp Val Lys Leu Gly Gly Val Leu Ser Gly Asn
 805 810 815

Asn Lys Lys Gln Leu Gln Gln Gly Thr Met Val Met Pro Asp Ile Leu
 820 825 830

30 Pro Glu Leu Met Pro Ser Asp Asn Thr Ile Lys Val Gly Ala Lys Gln
 835 840 845

Leu Pro Lys Ala Glu Phe Ser Lys Lys Asp Leu Lys Cys Val Ser Thr
 850 855 860

35 Ile Gln Ser Phe Arg Glu Arg Val Asn Ser Ile Ala Phe Phe Asp Asn
 865 870 875 880

	Gln Lys Leu Leu Cys Ala Gly Tyr Gly Asp Gly Thr Tyr Arg Val Phe	
	885	890 895
5	Asp Val Asn Asp Asn Trp Lys Cys Leu Tyr Thr Val Asn Gly His Arg	
	900	905 910
	Lys Ser Ile Glu Ser Ile Ala Cys Asn Ser Asn Tyr Ile Phe Thr Ser	
	915	920 925
10	Ser Pro Asp Asn Thr Ile Lys Val His Ile Ile Arg Ser Gly Asn Thr	
	930	935 940
	Lys Cys Ile Glu Thr Leu Val Gly His Thr Gly Glu Val Asn Cys Val	
	945	950 955 960
15	Val Ala Asn Glu Lys Tyr Leu Phe Ser Cys Ser Tyr Asp Lys Thr Ile	
	965	970 975
	Lys Val Trp Asp Leu Ser Thr Phe Lys Glu Ile Lys Ser Phe Glu Gly	
20	980	985 990
	Val His Thr Lys Tyr Ile Lys Thr Leu Ala Leu Ser Gly Arg Tyr Leu	
	995	1000 1005
25	Phe Ser Gly Gly Asn Asp-Gln Ile Ile Tyr Val Trp Asp Thr Glu Thr	
	1010	1015 1020
	Leu Ser Met Leu Phe Asn Met Gln Gly His Glu Asp Trp Val Leu Ser	
	1025	1030 1035 1040
30	Leu His Cys Thr Ala Ser Tyr Leu Phe Ser Thr Ser Lys Asp Asn Val	
	1045	1050 1055
	Ile Lys Ile Trp Asp Leu Ser Asn Phe Ser Cys Ile Asp Thr Leu Lys	
35	1060	1065 1070
	Gly His Trp Asn Ser Val Ser Ser Cys Val Val Lys Asp Arg Tyr Leu	

1075

1080

1085

Tyr Ser Gly Ser Glu Asp Asn Ser Ile Lys Val Trp Asp Leu Asp Thr
 1090 1095 1100

5

Leu Glu Cys Val Tyr Thr Ile Pro Lys Ser His Ser Leu Gly Val Lys
 1105 1110 1115 1120

10

Cys Leu Met Val Phe Asn Asn Gln Ile Ile Ser Ala Ala Phe Asp Gly
 1125 1130 1135

Ser Ile Lys Val Trp Glu Trp Gln Ser Lys
 1140 1145

15 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2237 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25 (iii) HYPOTHETICAL: NO ..

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Dictyostelium discoideum

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

35 ATAAGAAGAT AGAAGATGAT ATTTAAAGTT TGGTTTTTCAT ATGAAGATGA GGAAGTGGAA 60
 CTATCAGAAT TAACAAATGA TACAACAGTG TCAGCAATTA GAAAGATCTT ACATGAAGGT 120

	AAAATATTTA GATTTCATA TGGTACATCT CAAACAGACT TGCAAATTGG AAAGATGTTA	180
	CCATCTGGTA GTGGTGGAGG TGCAACTGCA GACAGCAAAT TTGAGAAGTT TAAAGCACGT	240
5	AATACATTAG CAGATATTCA ATATAAAGTT GGTGATACAT TATATGTTAG AGTTAAAAA	300
	AGTAAACCAA CAAATGATTC ATTATTACCA ACATTAAATA TAGCATTTTT AGATGGATCA	360
	GAACGTGCAA TTAAATGGGA ATATGACCCA TATACTACAA CTGCTCAATG GACCTGTACA	420
10	GCAACATTAG TCAAAGTTGA ACCAGTACCA TTTGCTGAAG GTGCATTTAG GAAAGCTTAT	480
	CATACATTGG ATTTAAGTAA ATCTGGTGCA AGTGGAAGAT ATGTATCAAA GATTGGTAAA	540
15	AAACCAACAC CAAGACCATC ATATTTTGAA GATGTAAAGA TGCAAATGAT AGCAAAGAAA	600
	TGGGCAGATA AATATAATTC ATTTAAACCT CCAAAAAAGA TTGAATTTTT ACAATCATGC	660
	GTTTTAGAGT TTGTAGATAG AACATCATCA GATTTAATTT GTGGAGCAGA ACCATATGTA	720
20	GAAGGACAAT ATAGAAAAGTA TAATAATAAT AGTGGATTCTG TTAGTAATGA TGAAAGAAAT	780
	ACACCACAAT CATCTCTCA TTTCACATAT GAACATTCAA ATCATCAATT ATTGATTATA	840
25	GATATTCAAG GTGTGGTGA TCACTATACA GACCCACAAA TTCATACCTA TGATGGTGTT	900
	GGTTTTGGTA TTGGTAATTT GGGTCAAAAA GGTTTTGAAA AGTTTTTAGA TACTCATAAA	960
	TGTAATGCAA TTTGCCAATA TTTAAATTTA CAATCAATTA ATCCAAAATC TGAAAAAGT	1020
30	GATTGTGGTA CTGTACCAAG ACCAGATTTA ATTTCCCTG ATACATCTGA AAGAGATAAT	1080
	AATAATAATA ATAATAATA TAATAATAAT AATAATAATA ATAATAATA TAATAGTAAT	1140
35	AATAATAATA ATAACAATAG TAGTATTTCA AAATCATTAG TTGAAATTC AAGTGGTAGT	1200
	AAAGAAAGAA ATGATAGAGA TTCGCCAAGT AGACAATTAT TTGTTTCAA TGATGGTAAT	1260

	ACATTAAATA CAAATAAAGA GAGATCAAAA TCAAAATCAA TAGATTTAGA AAAACCAGAA	1320
	ATTTTAATAA ATAATAAGAA AAAAGAGAGT ATAAATTTGG AAACGATAAA ATTAATTGAA	1380
5	ACTATTAAAG GATATCATGT TACAAGTCAT TTATGTATTT GTGATAATTT ATTATTTACA	1440
	GGATGTTTCA ATAATTCAAT TAGAGTGTAT GATTATAAGA GTCAAAATAT GGAATGTGTT	1500
	CAAACCTTGA AAGGTCATGA AGGTCCAGTT GAATCAATTT GTTATAATGA TCAATATTTG	1560
10	TTTAGTGGTT CATCAGATCA TTCAATTAAA GTTTGGGATT TAAAGAAATT AAGATGTATT	1620
	TTTACTTTGG AGGGTCATGA TAAACCTGTC CATACGGTTC TATTGAATGA TAAATATTTG	1680
15	TTTAGTGGTT CCTCTGACAA AACTATCAAA GTTTGGGATT TGAAAACTTT GGAATGTAAA	1740
	TATACCCTTG AAAGTCATGC CAGAGCCGTC AAAACACTTT GTATATCTGG TCAATATTTA	1800
	TTTAGTGGTT CAAATGATAA AACTATCAAG GTTTGGGATT TGAAAACTTT TCGTTGTAAC	1860
20	TACACTCTAA AAGGTCATAC TAAATGGGTC ACCACTATCT GTATATTAGG TACCAATCTC	1920
	TACAGTGGCT CCTATGATAA AACTATAAGA GTTTGGAATT TAAAGAGTTT AGAATGTTCC	1980
25	GCTACTTTAA GAGGCCATGA TAGATGSGTT GAACATATGG TAATTTGTGA TAAATTATTA	2040
	TTTACTGCTA GTGACGATAA TACAATTAAA ATTTGGGATT TAGAAACATT AAGATGTAAT	2100
	ACAACCTTGG AAGGACATAA TGCAACCGTT CAATGTTTAG CAGTTTGGGA AGATAAAAAA	2160
30	TGTGTTATTA GTTGTAGTCA TGATCAAAGT ATTAGAGTTT GGGGTTGGAA TTAATTTAAA	2220
	ATAAAAAAAA AAAACAT	2237
35	(2) INFORMATION FOR SEQ ID NO:8:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 732 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Dictyostelium discoideum

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ile Phe Lys Val Trp Phe Ser Tyr Glu Asp Glu Glu Val Glu Leu
 1 5 10 15

20

Ser Glu Leu Thr Asn Asp Thr Thr Val Ser Ala Ile Arg Lys Ile Leu
 20 25 30

His Glu Gly Lys Ile Phe Arg Phe Pro Tyr Gly Thr Ser Gln Thr Asp
 35 40 45

25

Leu Gln Ile Gly Lys Met Leu Pro Ser Gly Ser Gly Gly Gly Ala Thr
 50 55 60

30

Ala Asp Ser Lys Phe Glu Lys Phe Lys Ala Arg Asn Thr Leu Ala Asp
 65 70 75 80

Ile Gln Tyr Lys Val Gly Asp Thr Leu Tyr Val Arg Val Lys Lys Ser
 85 90 95

35

Lys Pro Thr Asn Asp Ser Leu Leu Pro Thr Leu Asn Ile Ala Phe Leu
 100 105 110

	Asp Gly Ser Glu Arg Ala Ile Lys Trp Glu Tyr Asp Pro Tyr Thr Thr	
	115	120 125
5	Thr Ala Gln Trp Thr Cys Thr Ala Thr Leu Val Lys Val Glu Pro Val	
	130	135 140
	Pro Phe Ala Glu Gly Ala Phe Arg Lys Ala Tyr His Thr Leu Asp Leu	
	145	150 155 160
10	Ser Lys Ser Gly Ala Ser Gly Arg Tyr Val Ser Lys Ile Gly Lys Lys	
		165 170 175
	Pro Thr Pro Arg Pro Ser Tyr Phe Glu Asp Val Lys Met Gln Met Ile	
		180 185 190
15	Ala Lys Lys Trp Ala Asp Lys Tyr Asn Ser Phe Lys Pro Pro Lys Lys	
		195 200 205
	Ile Glu Phe Leu Gln Ser Cys Val Leu Glu Phe Val Asp Arg Thr Ser	
20		210 215 220
	Ser Asp Leu Ile Cys Gly Ala Glu Pro Tyr Val Glu Gly Gln Tyr Arg	
	225	230 235 240
25	Lys Tyr Asn Asn Asn Ser Gly Phe Val Ser Asn Asp Glu Arg Asn Thr	
		245 250 255
	Pro Gln Ser Phe Ser His Phe Thr Tyr Glu His Ser Asn His Gln Leu	
		260 265 270
30	Leu Ile Ile Asp Ile Gln Gly Val Gly Asp His Tyr Thr Asp Pro Gln	
		275 280 285
	Ile His Thr Tyr Asp Gly Val Gly Phe Gly Ile Gly Asn Leu Gly Gln	
35		290 295 300
	Lys Gly Phe Glu Lys Phe Leu Asp Thr His Lys Cys Asn Ala Ile Cys	

	305		310		315		320
	Gln Tyr Leu Asn Leu Gln Ser Ile Asn Pro Lys Ser Glu Lys Ser Asp						
		325		330		335	
5							
	Cys Gly Thr Val Pro Arg Pro Asp Leu Ile Phe Pro Asp Thr Ser Glu						
		340		345		350	
10	Arg Asp Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn						
		355		360		365	
	Asn Asn Asn Asn Asn Ser Asn Asn Asn Asn Asn Asn Asn Ser Ser Ile						
		370		375		380	
15							
	Ser Lys Ser Leu Val Glu Ile Ser Ser Gly Ser Lys Glu Arg Asn Asp						
		385		390		395	400
	Arg Asp Ser Pro Ser Arg Gln Leu Phe Val Ser Asn Asp Gly Asn Thr						
		405		410		415	
20							
	Leu Asn Thr Asn Lys Glu Arg Ser Lys Ser Lys Ser Ile Asp Leu Glu						
		420		425		430	
	Lys Pro Glu Ile Leu Ile Asn Asn Lys Lys Lys Glu Ser Ile Asn Leu						
25		435		440		445	
	Glu Thr Ile Lys Leu Ile Glu Thr Ile Lys Gly Tyr His Val Thr Ser						
		450		455		460	
30							
	His Leu Cys Ile Cys Asp Asn Leu Leu Phe Thr Gly Cys Ser Asp Asn						
		465		470		475	480
	Ser Ile Arg Val Tyr Asp Tyr Lys Ser Gln Asn Met Glu Cys Val Gln						
		485		490		495	
35							
	Thr Leu Lys Gly His Glu Gly Pro Val Glu Ser Ile Cys Tyr Asn Asp						
		500		505		510	

Gln Tyr Leu Phe Ser Gly Ser Ser Asp His Ser Ile Lys Val Trp Asp
 515 520 525

5 Leu Lys Lys Leu Arg Cys Ile Phe Thr Leu Glu Gly His Asp Lys Pro
 530 535 540

Val His Thr Val Leu Leu Asn Asp Lys Tyr Leu Phe Ser Gly Ser Ser
 545 550 555 560

10 Asp Lys Thr Ile Lys Val Trp Asp Leu Lys Thr Leu Glu Cys Lys Tyr
 565 570 575

15 Thr Leu Glu Ser His Ala Arg Ala Val Lys Thr Leu Cys Ile Ser Gly
 580 585 590

Gln Tyr Leu Phe Ser Gly Ser Asn Asp Lys Thr Ile Lys Val Trp Asp
 595 600 605

20 Leu Lys Thr Phe Arg Cys Asn Tyr Thr Leu Lys Gly His Thr Lys Trp
 610 615 620

Val Thr Thr Ile Cys Ile Leu Gly Thr Asn Leu Tyr Ser Gly Ser Tyr
 625 630 635 640

25 Asp Lys Thr Ile Arg Val-Trp Asn Leu Lys Ser Leu Glu Cys Ser Ala
 645 650 655

Thr Leu Arg Gly His Asp Arg Trp Val Glu His Met Val Ile Cys Asp
 660 665 670

30 Lys Leu Leu Phe Thr Ala Ser Asp Asp Asn Thr Ile Lys Ile Trp Asp
 675 680 685

35 Leu Glu Thr Leu Arg Cys Asn Thr Thr Leu Glu Gly His Asn Ala Thr
 690 695 700

Val Gln Cys Leu Ala Val Trp Glu Asp Lys Lys Cys Val Ile Ser Cys

705

710

715

720

Ser His Asp Gln Ser Ile Arg Val Trp Gly Trp Asn

725

730

5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2307 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

15

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: C. elegans

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

25 ATGACGATCG ACACAACAAA TGAGAGCGAC AATAGTCCAA CTAAC TCACC AGGATTGGAG 60

GCCTCGGCTC GGACATTCTC GCTCAATGCG TCAAAAATGG TTCGGATAAC CGACGACTAC 120

GCAGATGAAG TGTTCAATTGA ACAGAATGAT GTCGTTATCG AGAAGCCTCG TATGGATCCT 180

30 CTCCACGTTA GAAAACTTAT GGAGACATGG CGCAAGGCTG CTCGCCGAGC AAGAACAAAC 240

TATATAGATC CATGGGATGA GTTCAACATC CACGAGTATC CAGTACAACG AGCTAAACGA 300

35 TATAGGTATT CTGCAATCAG AAAGCAATGG ACAGAGGATA TAGTCGATGT GAGACTTCAT 360

CCGGACAGTT TTGCACGTGG AGCCATGCCA GAATGCTACC GACTCAAAAA GTGCTCCAAG 420

	CACGGAACAA GTCAAGATTG GAGCAGCAAC TATGTCGCAA AAAGATACAT TTGTCAAGTC	480
	GATCGTAGAG TTCTTTTCGA TGATGTCAGA CTTCAGATGG ATGCCAAATT ATGGGCTGAA	540
5	GAATATAATC GGTATAATCC ACCGAAGAAA ATTGATATTG TTCAAATGTG TGTCAATTGAG	600
	ATGATTGATG TAAAAGGTTC TCCACTCTAT CATTGAGC ATTTTCATCGA GGGAAAATAT	660
	ATAAAATACA ATTCAAATC AGGATTTGTA TCAAATGCAG CTCGTCTTAC ACCACAAGCA	720
10	TTTTCTCACT TCACCTTCGA ACGTTCTGGT CATCAAATGA TGGTTGTCGA TATTCAAGGA	780
	GTTGGTGATC TTTACACAGA TCCTCAGATT CACACAGTTG TGGGAACTGA TTATGGAGAT	840
15	GGAAACCTCG GAACTCGTGG AATGGCTCTT TTCTTCATT CACACAGATG TAACGATATT	900
	TGTGAGACAA TGGATCTATC AAATTTGAA CTTTCGCCAC CTGAAATCGA GGCTACCGAA	960
	GTTGCGATGG AAGTAGCTGC AAAGCAGAAA AAGTCATGCA TAGTTCCTCC AACTGTGTTC	1020
20	GAAGCAAGAA GAAATCGAAT TTCAAGTGAA TGTGTACATG TCGAGCATGG TATTTGATG	1080
	GATCAATTGA GAAAAAGGAA GACGTTGAAT CAATCGTCAA CCGATTTGTC AGCAAAGAGT	1140
25	CACAACGAAG ACTGTGTATG TCCTGAGTGT ATTCCAGTTG TTGAGCAACT CTGTGAGCCT	1200
	TGCTCCGAAG ATGAAGAGGA CGAAGAAGAA GACTATCCAA GAAGTGAAAA AAGTGGAAT	1260
	AGTCAGAAAA GTCGACGTAG TAGAATGAGC ATTTCAACGA GATCTTCTGG CGATGAATCA	1320
30	GCATCTCGTC CTAGAAAATG CGGATTTGTA GATTTAACT CACTTCGTCA GAGACATGAT	1380
	AGCTTCAGAA GTTCTGTTGG GACATATTCT ATGAATAGTT CTAGACAAAC CAGAGACACT	1440
35	GAAAAGGATG AATTCTGGAA GGTTCCTCGA AAACAATCAG TTCCAGCAAA CATTCTATCA	1500
	CTTCAACTTC AACAAATGGC TGCTAACCTG GAAAATGATG AAGACGTACC ACAAGTCACC	1560

GGGCATCAGT TCTCTGTCCT CGGTCAGATT CATATTGATC TCTCACGATA TCATGAGCTC 1620

GGGCGGTTTCG TAGAAGTTGA TTCAGAACAT AAGGAAATGC TTGAGGGAAG TGAAAATGAC 1680

5 GCTCGTGTAC CAATCAAATA CGACAAGCAG TCTGCAATTT TCCATTGGA TATCGCTCGG 1740

AAGTGTGGAA TCCTTGAGGC TGTGCTAACA TCGGCTCATA TTGTTCTCGG ATTACCACAT 1800

GAATTGTTGA AAGAAGTCAC CGTTGATGAT CTGTTTCCTA ATGGGTTTGG AGAACAGGAA 1860

10 AATGGAATTC GAGCTGATAA AGGACAAAAA CCTTGTGACC TAGAAGAGTT CGGCTCCGAT 1920

CTGATGGAAT TTGCTGCAGA GATGGGTGAT AAGGGTGCAA TGCTGTACAT GGCACACGCT 1980

15 TATGAAACTG GTCAGCATCT CGGACCGAAT CGAAGAACGG ATTATAAGAA ATCGATTGAT 2040

TGGTATCAAC GCGTCGTTGG ATTCCAAGAA GAAGAAGAAC TTGACTCTGA TTGTGGAAAA 2100

ACGACATTCT CCTCATTTGC TCCACTGACT CGTCACGAGA TTCTAGCCAA AATGGCTGAA 2160

20 ATGTACAAAG AGGGAGGTTA TGGCCTGAAT CAAGACTTCG AACGAGCATA TGGTCTATTC 2220

AATGAAGCTG CTGAAGCAGC AATGGAAGCA ATGAATGGAA AGCTCGCAA TAAATACTAT 2280

25 GAAAAAGCGG AAATGTGTGG AGAATGA 2307

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 768 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *C. elegans*

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

10

Met Thr Ile Asp Thr Thr Asn Glu Ser Asp Asn Ser Pro Thr Asn Ser
 1 5 10 15

Pro Gly Leu Glu Ala Ser Ala Arg Thr Phe Ser Leu Asn Ala Ser Lys
 20 25 30

15

Met Val Arg Ile Thr Asp Asp Tyr Ala Asp Glu Val Phe Ile Glu Gln
 35 40 45

Asn Asp Val Val Ile Glu Lys Pro Arg Met Asp Pro Leu His Val Arg
 50 55 60

20

Lys Leu Met Glu Thr Trp Arg Lys Ala Ala Arg Arg Ala Arg Thr Asn
 65 70 75 80

Tyr Ile Asp Pro Trp Asp Glu Phe Asn Ile His Glu Tyr Pro Val Gln
 85 90 95

25

Arg Ala Lys Arg Tyr Arg Tyr Ser Ala Ile Arg Lys Gln Trp Thr Glu
 100 105 110

30

Asp Ile Val Asp Val Arg Leu His Pro Asp Ser Phe Ala Arg Gly Ala
 115 120 125

Met Arg Glu Cys Tyr Arg Leu Lys Lys Cys Ser Lys His Gly Thr Ser
 130 135 140

35

Gln Asp Trp Ser Ser Asn Tyr Val Ala Lys Arg Tyr Ile Cys Gln Val
 145 150 155 160

	Asp Arg Arg Val Leu Phe Asp Asp Val Arg Leu Gln Met Asp Ala Lys	
	165	170 175
5	Leu Trp Ala Glu Glu Tyr Asn Arg Tyr Asn Pro Pro Lys Lys Ile Asp	
	180	185 190
	Ile Val Gln Met Cys Val Ile Glu Met Ile Asp Val Lys Gly Ser Pro	
	195	200 205
10	Leu Tyr His Leu Glu His Phe Ile Glu Gly Lys Tyr Ile Lys Tyr Asn	
	210	215 220
	Ser Asn Ser Gly Phe Val Ser Asn Ala Ala Arg Leu Thr Pro Gln Ala	
	225	230 235 240
15	Phe Ser His Phe Thr Phe Glu Arg Ser Gly His Gln Met Met Val Val	
	245	250 255
	Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp Pro Gln Ile His Thr	
20	260	265 270
	Val Val Gly Thr Asp Tyr Gly Asp Gly Asn Leu Gly Thr Arg Gly Met	
	275	280 285
25	Ala Leu Phe Phe His Ser His Arg Cys Asn Asp Ile Cys Glu Thr Met	
	290	295 300
	Asp Leu Ser Asn Phe Glu Leu Ser Pro Pro Glu Ile Glu Ala Thr Glu	
	305	310 315 320
30	Val Ala Met Glu Val Ala Ala Lys Gln Lys Lys Ser Cys Ile Val Pro	
	325	330 335
	Pro Thr Val Phe Glu Ala Arg Arg Asn Arg Ile Ser Ser Glu Cys Val	
35	340	345 350
	His Val Glu His Gly Ile Ser Met Asp Gln Leu Arg Lys Arg Lys Thr	

	355	360	365
	Leu Asn Gln Ser Ser Thr Asp	Leu Ser Ala Lys Ser His Asn Glu Asp	
	370	375	380
5	Cys Val Cys Pro Glu Cys Ile Pro Val Val Glu Gln Leu Cys Glu Pro		
	385	390	395 400
	Cys Ser Glu Asp Glu Glu Asp Glu Glu Glu Asp Tyr Pro Arg Ser Glu		
10	405	410	415
	Lys Ser Gly Asn Ser Gln Lys Ser Arg Arg Ser Arg Met Ser Ile Ser		
	420	425	430
15	Thr Arg Ser Ser Gly Asp Glu Ser Ala Ser Arg Pro Arg Lys Cys Gly		
	435	440	445
	Phe Val Asp Leu Asn Ser Leu Arg Gln Arg His Asp Ser Phe Arg Ser		
	450	455	460
20	Ser Val Gly Thr Tyr Ser Met Asn Ser Ser Arg Gln Thr Arg Asp Thr		
	465	470	475 480
	Glu Lys Asp Glu Phe Trp Lys Val Leu Arg Lys Gln Ser Val Pro Ala		
25	485	490	495
	Asn Ile Leu Ser Leu Gln Leu Gln Gln Met Ala Ala Asn Leu Glu Asn		
	500	505	510
30	Asp Glu Asp Val Pro Gln Val Thr Gly His Gln Phe Ser Val Leu Gly		
	515	520	525
	Gln Ile His Ile Asp Leu Ser Arg Tyr His Glu Leu Gly Arg Phe Val		
	530	535	540
35	Glu Val Asp Ser Glu His Lys Glu Met Leu Glu Gly Ser Glu Asn Asp		
	545	550	555 560

	Ala Arg Val Pro Ile Lys Tyr Asp Lys Gln Ser Ala Ile Phe His Leu	
	565	570 575
5	Asp Ile Ala Arg Lys Cys Gly Ile Leu Glu Ala Val Leu Thr Ser Ala	
	580	585 590
	His Ile Val Leu Gly Leu Pro His Glu Leu Leu Lys Glu Val Thr Val	
	595	600 605
10	Asp Asp Leu Phe Pro Asn Gly Phe Gly Glu Gln Glu Asn Gly Ile Arg	
	610	615 620
	Ala Asp Lys Gly Gln Lys Pro Cys Asp Leu Glu Glu Phe Gly Ser Asp	
	625	630 635 640
15	Leu Met Glu Ile Ala Ala Glu Met Gly Asp Lys Gly Ala Met Leu Tyr	
	645	650 655
	Met Ala His Ala Tyr Glu Thr Gly Gln His Leu Gly Pro Asn Arg Arg	
20	660	665 670
	Thr Asp Tyr Lys Lys Ser Ile Asp Trp Tyr Gln Arg Val Val Gly Phe	
	675	680 685
25	Gln Glu Glu Glu Glu Leu Asp Ser Asp Cys Gly Lys Thr Thr Phe Ser	
	690	695 700
	Ser Phe Ala Pro Leu Thr Arg His Glu Ile Leu Ala Lys Met Ala Glu	
	705	710 715 720
30	Met Tyr Lys Glu Gly Gly Tyr Gly Leu Asn Gln Asp Phe Glu Arg Ala	
	725	730 735
	Tyr Gly Leu Phe Asn Glu Ala Ala Glu Ala Ala Met Glu Ala Met Asn	
35	740	745 750
	Gly Lys Leu Ala Asn Lys Tyr Tyr Glu Lys Ala Glu Met Cys Gly Glu	

755

760

765

(2) INFORMATION FOR SEQ ID NO:11:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2283 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: C. elegans

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGACGATCG ACACAACAAA TGAGAGCGAC AATAGTCCAA CTAAC TCACC AGGATTGGAG 60

25 GCCTCGGCTC GGACATTCTC GCTCAATGCG TCAAAAATGG TTCGGATAAC CGACGACTAC 120

GCAGATGAAG TGTTCATTGA ACAGAATGAT GTCGTTATCG AGAAGCCTCG TATGGATCCT 180

CTCCACGTTA GAAAACTTAT GGAGACATGG CGCAAGGCTG CTCGCCGAGC AAGAACAAAC 240

30

TATATAGATC CATGGGATGA GTTCAACATC CACGAGTATC CAGTACAACG AGCTAAACGA 300

TATAGGTATT CTGCAATCAG AAAGCAATGG ACAGAGGATA TAGTCGATGT GAGACTTCAT 360

35 CCGGACAGTT TTGCACGTGG AGCCATGCGA GAATGCTACC GACTCAAAAA GTGCTCCAAG 420

CACGGAACAA GTCAAGATTG GAGCAGCAAC TATGTCGCAA AAAGATACAT TTGTCAAGTC 480

	GATCGTAGAG TTCTTTTCGA TGATGTCAGA CTTCAGATGG ATGCCAAATT ATGGGCTGAA	540
	GAATATAATC GGTATAATCC ACCGAAGAAA ATTGATATTG TTCAAATGTG TGTCAATTGAG	600
5	ATGATTGATG TAAAAGGTTC TCCACTCTAT CATTGGAGC ATTTTCATCGA GGGAAAATAT	660
	ATAAAATACA ATTCAAACCTC AGGATTTGTA TCAAATGCAG CTCGTCTTAC ACCACAAGCA	720
	TTTTCTCACT TCACCTTCGA ACGTTCTGGT CATCAAATGA TGGTTGTCGA TATTCAAGGA	780
10	GTTGGTGATC TTTACACAGA TCCTCAGATT CACACAGTTG TGGGAACTGA TTATGGAGAT	840
	GGAAACCTCG GAACTCGTGG AATGGCTCTT TTCTTCCATT CACACAGATG TAACGATATT	900
15	TGTGAGACAA TGGATCTATC AAATTTTCGAA CTTTCGCCAC CTGAAATCGA GGCTACCGAA	960
	GTTGCGATGG AAGTAGCTGC AAAGCAGAAA AAGTCATGCA TAGTTCCTCC AACTGTGTTC	1020
	GAAGCAAGAA GAAATCGAAT TTCAAGTGAA TGTGTACATG TCGAGCATGG TATTTTCGATG	1080
20	GATCAATTGA GAAAAAGGAA GACGTTGAAT CAATCGTCAA CCGATTTGTC AGCAAAGAGT	1140
	CACAACGAAG ACTGTGTATG TCCTGAGTGT ATTCCAGTTG TTGAGCAACT CTGTGAGCCT	1200
25	TGCTCCGAAG ATGAAGAGGA CGAAGAAGAA GACTATCCAA GAAGTGAAAA AAGTGGAAT	1260
	AGTCAGAAAA GTCGACGTAG TAGAATGAGC ATTTCAACGA GATCTTCTGG CGATGAATCA	1320
	GCATCTCGTC CTAGAAAATG CGGATTTGTA GATTTAACT CACTTCGTCA GAGACATGAT	1380
30	AGCTTCAGAA GTTCTGTTGG GACATATTCT ATGAATAGTT CTAGACAAAC CAGAGACACT	1440
	GAAAAGGATG AATTCTGGAA GGTTCCTTCGA AAACAATCAG TTCCAGCAAA CATTCTATCA	1500
35	CTTCAACTTC AACAAATGGC TGCTAACCTG GAAAATGATG AAGACGTACC ACAAGTCACC	1560
	GGGCATCAGT TCTCTGTCCT CGGTCAGATT CATATTGATC TCTCACGATA TCATGAGCTC	1620

GGGCGGTTTCG TAGAAGTTGA TTCAGAACAT AAGGAAATGC TTGAGGGAAG TGAAAATGAC 1680

GCTCGTGTAC CAATCAAATA CGACAAGCAG TCTGCAATTT TCCATTTGGA TATCGCTCGG 1740

5 AAGTGTGGAA TCCTTGAGGC TGTGCTAACA TCGGCTCATA TTGTTCTCGG ATTACCACAT 1800

GAATTGTTGA AAGAAGTCAC CGTTGATGAT CTGTTTCCTA ATGGGTTTGG AGAACAGGAA 1860

AATGGAATTC GAGACCTAGA AGAGTTCGGC TCCGATCTGA TGGAAATTGC TGCAGAGATG 1920

10 GGTGATAAGG GTGCAATGCT GTACATGGCA CACGCTTATG AACTGGTCA GCATCTCGGA 1980

CCGAATCGAA GAACGGATTA TAAGAAATCG ATTGATTGGT ATCAACGCGT CGTTGGATTC 2040

15 CAAGAAGAAG AAGAACTTGA CTCTGATTGT GGAAAAACGA CATTCTCCTC ATTTGCTCCA 2100

CTGACTCGTC ACGAGATTCT AGCCAAAATG GCTGAAATGT ACAAAGAGGG AGGTTATGGC 2160

CTGAATCAAG ACTTCGAACG AGCATATGGT CTATTCAATG AAGCTGCTGA AGCAGCAATG 2220

20 GAAGCAATGA ATGGAAAGCT CGCAAATAAA TACTATGAAA AAGCGGAAAT GTGTGGAGAA 2280

TGA 2283

25 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 amino acids
- (B) TYPE: amino acid
- 30 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *C. elegans*

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Thr Ile Asp Thr Thr Asn Glu Ser Asp Asn Ser Pro Thr Asn Ser
 1 5 10 15

10 Pro Gly Leu Glu Ala Ser Ala Arg Thr Phe Ser Leu Asn Ala Ser Lys
 20 25 30

Met Val Arg Ile Thr Asp Asp Tyr Ala Asp Glu Val Phe Ile Glu Gln
 35 40 45

15 Asn Asp Val Val Ile Glu Lys Pro Arg Met Asp Pro Leu His Val Arg
 50 55 60

20 Lys Leu Met Glu Thr Trp Arg Lys Ala Ala Arg Arg Ala Arg Thr Asn
 65 70 75 80

Tyr Ile Asp Pro Trp Asp Glu Phe Asn Ile His Glu Tyr Pro Val Gln
 85 90 95

25 Arg Ala Lys Arg Tyr Arg-Tyr Ser Ala Ile Arg Lys Gln Trp Thr Glu
 100 105 110

Asp Ile Val Asp Val Arg Leu His Pro Asp Ser Phe Ala Arg Gly Ala
 115 120 125

30 Met Arg Glu Cys Tyr Arg Leu Lys Lys Cys Ser Lys His Gly Thr Ser
 130 135 140

35 Gln Asp Trp Ser Ser Asn Tyr Val Ala Lys Arg Tyr Ile Cys Gln Val
 145 150 155 160

Asp Arg Arg Val Leu Phe Asp Asp Val Arg Leu Gln Met Asp Ala Lys

	165	170	175
	Leu Trp Ala Glu Glu Tyr Asn Arg Tyr Asn Pro Pro Lys Lys Ile Asp		
	180	185	190
5	Ile Val Gln Met Cys Val Ile Glu Met Ile Asp Val Lys Gly Ser Pro		
	195	200	205
	Leu Tyr His Leu Glu His Phe Ile Glu Gly Lys Tyr Ile Lys Tyr Asn		
10	210	215	220
	Ser Asn Ser Gly Phe Val Ser Asn Ala Ala Arg Leu Thr Pro Gln Ala		
	225	230	235 240
15	Phe Ser His Phe Thr Phe Glu Arg Ser Gly His Gln Met Met Val Val		
	245	250	255
	Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp Pro Gln Ile His Thr		
20	260	265	270
	Val Val Gly Thr Asp Tyr Gly Asp Gly Asn Leu Gly Thr Arg Gly Met		
	275	280	285
	Ala Leu Phe Phe His Ser His Arg Cys Asn Asp Ile Cys Glu Thr Met		
25	290	295	300
	Asp Leu Ser Asn Phe Glu Leu Ser Pro Pro Glu Ile Glu Ala Thr Glu		
	305	310	315 320
30	Val Ala Met Glu Val Ala Ala Lys Gln Lys Lys Ser Cys Ile Val Pro		
	325	330	335
	Pro Thr Val Phe Glu Ala Arg Arg Asn Arg Ile Ser Ser Glu Cys Val		
35	340	345	350
	His Val Glu His Gly Ile Ser Met Asp Gln Leu Arg Lys Arg Lys Thr		
	355	360	365

	Leu Asn Gln Ser Ser Thr Asp Leu Ser Ala Lys Ser His Asn Glu Asp
	370 375 380
5	Cys Val Cys Pro Glu Cys Ile Pro Val Val Glu Gln Leu Cys Glu Pro
	385 390 395 400
	Cys Ser Glu Asp Glu Glu Asp Glu Glu Glu Asp Tyr Pro Arg Ser Glu
	405 410 415
10	Lys Ser Gly Asn Ser Gln Lys Ser Arg Arg Ser Arg Met Ser Ile Ser
	420 425 430
	Thr Arg Ser Ser Gly Asp Glu Ser Ala Ser Arg Pro Arg Lys Cys Gly
15	435 440 445
	Phe Val Asp Leu Asn Ser Leu Arg Gln Arg His Asp Ser Phe Arg Ser
	450 455 460
	Ser Val Gly Thr Tyr Ser Met Asn Ser Ser Arg Gln Thr Arg Asp Thr
20	465 470 475 480
	Glu Lys Asp Glu Phe Trp Lys Val Leu Arg Lys Gln Ser Val Pro Ala
	485 490 495
25	Asn Ile Leu Ser Leu Gln Leu Gln Gln Met Ala Ala Asn Leu Glu Asn
	500 505 510
	Asp Glu Asp Val Pro Gln Val Thr Gly His Gln Phe Ser Val Leu Gly
30	515 520 525
	Gln Ile His Ile Asp Leu Ser Arg Tyr His Glu Leu Gly Arg Phe Val
	530 535 540
	Glu Val Asp Ser Glu His Lys Glu Met Leu Glu Gly Ser Glu Asn Asp
35	545 550 555 560
	Ala Arg Val Pro Ile Lys Tyr Asp Lys Gln Ser Ala Ile Phe His Leu

565

570

575

Asp Ile Ala Arg Lys Cys Gly Ile Leu Glu Ala Val Leu Thr Ser Ala
580 585 590

5

His Ile Val Leu Gly Leu Pro His Glu Leu Leu Lys Glu Val Thr Val
595 600 605

10

Asp Asp Leu Phe Pro Asn Gly Phe Gly Glu Gln Glu Asn Gly Ile Arg
610 615 620

Asp Leu Glu Glu Phe Gly Ser Asp Leu Met Glu Ile Ala Ala Glu Met
625 630 635 640

15

Gly Asp Lys Gly Ala Met Leu Tyr Met Ala His Ala Tyr Glu Thr Gly
645 650 655

Gln His Leu Gly Pro Asn Arg Arg Thr Asp Tyr Lys Lys Ser Ile Asp
660 665 670

20

Trp Tyr Gln Arg Val Val Gly Phe Gln Glu Glu Glu Glu Leu Asp Ser
675 680 685

25

Asp Cys Gly Lys Thr Thr Phe Ser Ser Phe Ala Pro Leu Thr Arg His
690 695 700

Glu Ile Leu Ala Lys Met Ala Glu Met Tyr Lys Glu Gly Gly Tyr Gly
705 710 715 720

30

Leu Asn Gln Asp Phe Glu Arg Ala Tyr Gly Leu Phe Asn Glu Ala Ala
725 730 735

Glu Ala Ala Met Glu Ala Met Asn Gly Lys Leu Ala Asn Lys Tyr Tyr
740 745 750

35

Glu Lys Ala Glu Met Cys Gly Glu
755 760

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 628 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: Dictyostelium discoideum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

20 GTATTGTATG TGTTTCAATT GAGAAGACTC CATTTGCAAA GGGTAGTTGT AGAACAGCAC 60
ATAAATTAAA GGATTGGAGT CAACCAGATC AAGGATTAGT TGGTAAATTT TCAACCAATA 120
AAAAGACGAC AAGAGATTCA TACTTTACAG ATGTATTGAT GCAAACATTT TGTGCTAAAT 180
25 GGGCAGAGAA ATTCAATGAA GCGAAACCAC CAAAACCAAT TACATTCTTA CCATCATACG 240
TTTACGAATT GATTGATCAT CCACCACCTT ATCCAGTTTG TGGTGGTGAA CCATTCATTG 300
30 AGGGAGATTA CAAGAAACAT AACAACAACA GTGGTTACGT TAGTAGTGAT GCTAGAAATA 360
CACCACAATC ATTCTCTCAT TTCTCATACG AACTCTCCAA TCATGAATTG TTGATCGTTG 420
ATATCCAAGG TGTCAACGAT TTCTTACTG ATCCTCAAAT TCATACGAAA TCAGGCGAGG 480
35 GCTTTGGCGA GGGTAATTTG GCGAGACGG GTTCCACAA ATTCCTTCAA ACACACAAGT 540

GTAATCCAGT TTGTGACTTT TTAAAGTTGA AACCAATCAA TCAATCAAAG AAAGCCCTCC 600

TAAGAGGTAC ATTACCCGTC GTACAATT 628

5 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 209 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Dictyostelium discoideum

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

25 Ile Val Cys Val Ser Ile Glu Lys Thr Pro Phe Ala Lys Gly Ser Cys
1 5 10 15

Arg Thr Ala His Lys Leu Lys Asp Trp Ser Gln Pro Asp Gln Gly Leu
20 25 30

30 Val Gly Lys Phe Ser Thr Asn Lys Lys Thr Thr Arg Asp Ser Tyr Phe
35 40 45

Thr Asp Val Leu Met Gln Thr Phe Cys Ala Lys Trp Ala Glu Lys Phe
50 55 60

35

Asn Glu Ala Lys Pro Pro Lys Pro Ile Thr Phe Leu Pro Ser Tyr Val
65 70 75 80

Tyr Glu Leu Ile Asp His Pro Pro Pro Tyr Pro Val Cys Gly Gly Glu
 85 90 95
 Pro Phe Ile Glu Gly Asp Tyr Lys Lys His Asn Asn Asn Ser Gly Tyr
 5 100 105 110
 Val Ser Ser Asp Ala Arg Asn Thr Pro Gln Ser Phe Ser His Phe Ser
 115 120 125
 Tyr Glu Leu Ser Asn His Glu Leu Leu Ile Val Asp Ile Gln Gly Val
 10 130 135 140
 Asn Asp Phe Tyr Thr Asp Pro Gln Ile His Thr Lys Ser Gly Glu Gly
 145 150 155 160
 Phe Gly Glu Gly Asn Leu Gly Glu Thr Gly Phe His Lys Phe Leu Gln
 15 165 170 175
 Thr His Lys Cys Asn Pro Val Cys Asp Phe Leu Lys Leu Lys Pro Ile
 20 180 185 190
 Asn Gln Ser Lys Lys Ala Leu Leu Arg Gly Thr Leu Pro Val Val Gln
 195 200 205
 25 Leu

(2) INFORMATION FOR SEQ ID NO:15:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

10 Gly Glu Trp Leu Asp Asp Glu Val Leu Ile Lys Met Ala Ser Gln Pro
1 5 10 15

Phe Gly Arg Gly Ala Met Arg Glu Cys Phe Arg Thr Lys Lys Leu Ser
20 25 30

15 Asn Phe Leu His Ala Gln Gln Trp Lys Gly Ala Ser Asn Tyr Val Ala
35 40 45

Lys Arg Tyr Ile Glu Pro Val Asp Arg Asp Val Tyr Phe Glu Asp Val
20 50 55 60

Arg Leu Gln Met Glu Ala Lys Leu Trp Gly Glu Glu Tyr Asn Arg His
65 70 75 80

25 Lys Pro Pro Lys Gln Val Asp Ile Met Gln Met Cys Ile Ile Glu Leu
85 90 95

Lys Asp Arg Pro Gly Lys Pro Leu Phe His Leu Glu His Tyr Ile Glu
100 105 110

30 Gly Lys Tyr Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Arg Asp Asp
115 120 125

Asn Ile Arg Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg
130 135 140

Ser Gly His Gln Leu Ile Val Val Asp Ile Gln Gly Val Gly Asp Leu

145 150 155 160

Tyr Thr Asp Pro Gln Ile His Thr Glu Thr Gly Thr Asp Phe Gly Asp
165 170 175

5

Gly Asn Leu Gly Val Arg Gly Met Ala Leu Phe Phe Tyr Ser His Ala
180 185 190

10

Cys Asn Arg Ile Cys Glu Ser Met Gly Leu Ala Pro Phe Asp Leu Ser
195 200 205

Pro Arg Glu Arg Asp Ala Val Asn Gln Asn Thr Lys Leu Leu Gln Ser
210 215 220

15

Ala Lys Thr Ile Leu Arg Gly Thr Glu Glu Lys Cys Gly Ser
225 230 235

(2) INFORMATION FOR SEQ ID NO:16:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

30

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: D. discoideum

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn Lys Trp Ile Arg Leu Ser Met Lys Leu Lys Val Glu Arg Lys Pro

	1	5	10	15
	Phe	Ala	Glu	Gly
		Ala	Leu	Arg
		Glu	Ala	Tyr
		His	Thr	Val
		Ser	Leu	Gly
		20	25	30
5	Val	Gly	Thr	Asp
		Glu	Asn	Tyr
		Pro	Leu	Gly
		Thr	Thr	Thr
		Lys	Leu	Phe
		35	40	45
	Pro	Pro	Ile	Glu
		Met	Ile	Ser
		Pro	Ile	Ser
		Lys	Asn	Asn
		Glu	Ala	Met
10		50	55	60
	Thr	Gln	Leu	Lys
		Asn	Gly	Thr
		Lys	Phe	Val
		Leu	Lys	Leu
		Tyr	Lys	Lys
	65	70	75	80
	Glu	Ala	Glu	Gln
		Gln	Ala	Ser
		Arg	Glu	Leu
		Tyr	Phe	Glu
		Asp	Val	Lys
15		85	90	95
	Met	Gln	Met	Val
		Cys	Arg	Asp
		Trp	Gly	Asn
		Lys	Phe	Asn
		Gln	Lys	Lys
		100	105	110
20	Pro	Pro	Lys	Lys
		Ile	Glu	Phe
		Leu	Met	Ser
		Trp	Val	Val
		Glu	Leu	Ile
		115	120	125
	Asp	Arg	Ser	Pro
		Ser	Ser	Asn
		Gly	Gln	Pro
		Ile	Leu	Cys
		Ser	Ile	Glu
25		130	135	140
	Pro	Leu	Leu	Val
		Gly	Glu	Phe
		Lys	Lys	Asn
		Asn	Ser	Asn
		Tyr	Gly	Ala
	145	150	155	160
	Val	Leu	Thr	Asn
		Arg	Ser	Thr
		Pro	Gln	Ala
		Phe	Ser	His
		Phe	Thr	Tyr
30		165	170	175
	Glu	Leu	Ser	Asn
		Lys	Gln	Met
		Ile	Val	Val
		Asp	Ile	Gln
		Gly	Val	Asp
		180	185	190
35	Asp	Leu	Tyr	Thr
		Asp	Pro	Gln
		Ile	His	Thr
		Pro	Asp	Gly
		Lys	Gly	Phe
		195	200	205

Gly Leu Gly Asn Leu Gly Lys Ala Gly Ile Asn Lys Phe Ile Thr Thr
 210 215 220

5 His Lys Cys Asn Ala Val Cys Ala Leu Leu Asp Leu Asp Val Lys Leu
 225 230 235 240

Gly Gly Val Leu Ser Gly Asn Asn Lys Lys Gln Leu Gln Gln Gly Thr
 245 250 255

10 Met Val

(2) INFORMATION FOR SEQ ID NO:17:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: D. discoideum

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala Gln Trp Thr Cys Thr Ala Thr Leu Val Lys Val Glu Pro Val Pro
 1 5 10 15

35 Phe Ala Glu Gly Ala Phe Arg Lys Ala Tyr His Thr Leu Asp Leu Ser
 20 25 30

	Lys Ser Gly Ala Ser Gly Arg Tyr Val Ser Lys Ile Gly Lys Lys Pro	
	35	40 45
5	Thr Pro Arg Pro Ser Tyr Phe Glu Asp Val Lys Met Gln Met Ile Ala	
	50	55 60
	Lys Lys Trp Ala Asp Lys Tyr Asn Ser Phe Lys Pro Pro Lys Lys Ile	
	65	70 75 80
10	Glu Phe Leu Gln Ser Cys Val Leu Glu Phe Val Asp Arg Thr Ser Ser	
		85 90 95
	Asp Leu Ile Cys Gly Ala Glu Pro Tyr Val Glu Gly Gln Tyr Arg Lys	
		100 105 110
15	Tyr Asn Asn Asn Ser Gly Phe Val Ser Asn Asp Glu Arg Asn Thr Pro	
		115 120 125
	Gln Ser Phe Ser His Phe Thr Tyr Glu His Ser Asn His Gln Leu Leu	
20		130 135 140
	Ile Ile Asp Ile Gln Gly Val Gly Asp His Tyr Thr Asp Pro Gln Ile	
	145	150 155 160
25	His Thr Tyr Asp Gly Val Gly Phe Gly Ile Gly Asn Leu Gly Gln Lys	
		165 170 175
	Gly Phe Glu Lys Phe Leu Asp Thr His Lys Cys Asn Ala Ile Cys Gln	
		180 185 190
30	Tyr Leu Asn Leu Gln Ser Ile Asn Pro Lys Ser Glu Lys Ser Asp Cys	
		195 200 205
	Gly Thr Val Pro	
35		210

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: C. elegans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Gln Trp Thr Glu Asp Ile Val Asp Val Arg Leu His Pro Asp Ser
 1 5 10 15

Phe Ala Arg Gly Ala Met Arg Glu Cys Tyr Arg Leu Lys Lys Cys Ser
 20 25 30

Lys His Gly Thr Ser Gln Asp Trp Ser Ser Asn Tyr Val Ala Lys Arg
 25 35 40 45

Tyr Ile Cys Gln Val Asp Arg Arg Val Leu Phe Asp Asp Val Arg Leu
 50 55 60

Gln Met Asp Ala Lys Leu Trp Ala Glu Glu Tyr Asn Arg Tyr Asn Pro
 65 70 75 80

Pro Lys Lys Ile Asp Ile Val Gln Met Cys Val Ile Glu Met Ile Asp
 85 90 95

Val Lys Gly Ser Pro Leu Tyr His Leu Glu His Phe Ile Glu Gly Lys
 100 105 110

Tyr Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Ser Asn Ala Ala Arg
 115 120 125

5 Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His
 130 135 140

Gln Met Met Val Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp
 145 150 155 160

10 Pro Gln Ile His Thr Val Val Gly Thr Asp Tyr Gly Asp Gly Asn Leu
 165 170 175

Gly Thr Arg Gly Met Ala Leu Phe Phe His Ser His Arg Cys Asn Asp
 180 185 190

15 Ile Cys Glu Thr Met Asp Leu Ser Asn Phe Glu Leu Ser Pro Pro Glu
 195 200 205

20 Ile Glu Ala Thr Glu Val Ala Met Glu Val Ala Ala Lys Gln Lys Lys
 210 215 220

Ser Cys Ile Val Pro Pro Thr Val Phe
 225 230

25 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35 (A) DESCRIPTION: /desc = "Oligonucleotide Primer D"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5 GGATTGGAC TGGACAAGAA CCCCC

25

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

25 Arg Lys Lys Phe Gly Glu Ser Glu Lys Thr Lys Thr Lys Glu Phe Leu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:21:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg
1 5 10

10

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

15

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20

(iii) HYPOTHETICAL: NO

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Ala Asn Xaa Tyr Tyr Glu Lys Ala Glu
1 5 10

30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

10

CANGCNTTNN NNCANTTNAC NTTNGANNG

29

(2) INFORMATION FOR SEQ ID NO:24:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

30

TCNGCNTTNT CNTANTANTT NTTNGC

26

(2) INFORMATION FOR SEQ ID NO:25:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TACAATCAGC TGATGACCAG AACGCTC

27

15